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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=11; day=7; hr=10; min=17; sec=31; ms=149;]

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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=10; day=10; hr=15; min=28; sec=11; ms=868;
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Application No: 10585077 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-10-07 15:13:25.344
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 988 ms
Total Warnings: 13
Total Errors: 0
No. of SeqIDs Defined: 32
Actual SeqID Count: 32

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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)

SEQUENCE LISTING

<110> CHRISTENSEN, GEIR
ANDERSSON, KRISTIN BREVIK

<120> NON-HUMAN MAMMAL COMPRISING A MODIFIED SERCA2 GENE AND
METHODS, CELLS, GENES, AND VECTORS THEREOF

<130> 3657-1037

<140> 10585077
<141> 2008-10-07

<150> PCT/NO04/000397

<151> 2004-12-22

<150> 60/533,740

<151> 2003-12-30

<160> 32

<170> PatentIn Ver. 3.3

<210> 1
<211> 801
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 1

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acccggctcc acctctgtggg gcttggctcg ggcgc当地 cgc当地 gagaggccgg 180
cggtccacgc gcgggtctgg gccatcgccc accttagggg tctc当地 atca agcttatcga 240
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ggctgggctg agtccccccgc ggattttatga ggc当地 cgtc当地 ttgtt当地 gagaa accctc当地 ggac 540
cgttt当地 ttgt gtc当地 cccaaa gttgc当地 acatc tggc当地 gagat gatgacccag ctgaaatgac 600
tgc当地 atggtcc tggaggccgg agagggctta cgggc当地 gttc cgaggccact gattaccagg 660
gctg当地 ataataat tt当地 ctgggg tatcaaagtg gagacagatt gttgtacgtt catacaccta 720
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<210> 2
<211> 803
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

nucleotide construct

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gtttaagtct gaccagggg gatccggAAC ccttaatata acttcgtata atgtatgcta 180
tacgaagtta ttaggtccct cgacctgcag cccaaGCTGA tcctctagtc gagccccAGC 240
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cttccagggt caaggaaggc acgggggagg ggcaaacaac agatggctgg caactagaag 480
gcacagtcgaa ggctgatcg cgagctctag cttagaaatt gatccccatc gaagaactcg 540
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tgtctgataa gcggtccgccc cacacccaac cggccacaag tcatgaaatc caaaaaagcg 720
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<210> 3

<211> 860

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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cgagaacgcg cagcctggtc gaacgcagac gcgtgttgat ggcggggta cgaagccata 360
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tcgaattcgc caatgacaag acgcgtggcg gggtttgcgc gacattgggt ggaaacattc 600
caggcctggg tggagaggct ttttgcgttcc tcttgcaaaa ccacactgct cgacattggg 660
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cgatccggaa cccttaatat aacttcgtat aatgtatgct atacgaagtt attaggtccc 780
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<210> 4

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 4

ataacttcgt ataatgtatg ctatacgaag ttat

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 5
ccaaggaaga tggctgacc 19

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 6
catcgacgcc tcataaatcc 20

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 7
tcttcataaac acacgccaat tt 22

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 8
ccctttgctg ccaattaact att 23

<210> 9
<211> 21
<212> DNA

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 9
acctcttaggg gtctcgaaatc a

21

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 10
aagttgaata accggaaatg gttt

24

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic primer

<400> 11
tgttataagg aatccccaga aatg

24

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic primer

<400> 12
aggctccctcg aactctccag

20

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 13

gtaagagagc ttcccttcctc ctt

23

<210> 14

<211> 994

<212> PRT

<213> Mus musculus

<400> 14

Met Glu Ala Ala His Ser Lys Ser Thr Glu Glu Cys Leu Ser Tyr Phe
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Gly Val Ser Glu Thr Thr Gly Leu Thr Pro Asp Gln Val Lys Arg His
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Leu Glu Lys Tyr Gly Pro Asn Glu Leu Pro Ala Glu Glu Gly Lys Ser
35 40 45

Leu Trp Glu Leu Val Val Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
50 55 60

Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65 70 75 80

Gly Glu Glu Thr Val Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
85 90 95

Ile Leu Ile Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125

Val Tyr Arg Ala Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Arg Asp
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Val Ala Val Gly Asp Lys Val Pro
145 150 155 160

Ala Asp Ile Arg Ile Leu Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Val Gly Ile Val Ala
210 215 220

Thr Thr Gly Val Ser Thr Glu Ile Gly Lys Ile Arg Asp Gln Met Ala
225 230 235 240

Ala Thr Glu Gln Asp Lys Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe

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Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Val Ala Val Trp			
260	265	270	
Leu Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp			
275	280	285	
Phe Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val			
290	295	300	
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala			
305	310	315	320
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu			
325	330	335	
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys			
340	345	350	
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Lys Met Phe Ile			
355	360	365	
Ile Asp Lys Val Asp Gly Asp Val Cys Ser Leu Asn Glu Phe Ser Ile			
370	375	380	
Thr Gly Ser Thr Tyr Ala Pro Glu Gly Glu Val Leu Lys Asn Asp Lys			
385	390	395	400
Pro Val Arg Ala Gly Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile			
405	410	415	
Cys Ala Leu Cys Asn Asp Ser Ser Leu Asp Phe Asn Glu Thr Lys Gly			
420	425	430	
Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Thr Leu			
435	440	445	
Val Glu Lys Met Asn Val Phe Asn Thr Glu Val Arg Ser Leu Ser Lys			
450	455	460	
Val Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Arg Gln Leu Met Lys			
465	470	475	480
Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val			
485	490	495	
Tyr Cys Ser Pro Ala Lys Ser Ser Arg Ala Ala Val Gly Asn Lys Met			
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Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Asn Tyr Val			
515	520	525	
Arg Val Gly Thr Thr Arg Val Pro Leu Thr Gly Pro Val Lys Glu Lys			
530	535	540	
Ile Met Ser Val Ile Lys Glu Trp Gly Thr Gly Arg Asp Thr Leu Arg			

545 550 555 560
Cys Leu Ala Leu Ala Thr Arg Asp Thr Pro Pro Lys Arg Glu Glu Met
565 570 575

Val Leu Asp Asp Ser Ala Lys Phe Met Glu Tyr Glu Met Asp Leu Thr
580 585 590

Phe Val Gly Val Val Gly Met Leu Asp Pro Pro Arg Lys Glu Val Thr
595 600 605

Gly Ser Ile Gln Leu Cys Arg Asp Ala Gly Ile Arg Val Ile Met Ile
610 615 620

Thr Gly Asp Asn Lys Gly Thr Ala Ile Ala Ile Cys Arg Arg Ile Gly
625 630 635 640

Ile Phe Ser Glu Asn Glu Glu Val Thr Asp Arg Ala Tyr Thr Gly Arg
645 650 655

Glu Phe Asp Asp Leu Pro Leu Ala Glu Gln Arg Glu Ala Cys Arg Arg
660 665 670

Ala Cys Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val
675 680 685

Glu Tyr Leu Gln Ser Tyr Asp Glu Ile Thr Ala Met Thr Gly Asp Gly
690 695 700

Val Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met
705 710 715 720

Gly Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala
725 730 735

Asp Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala
740 745 750

Ile Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn
755 760 765

Val Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Leu Pro
770 775 780

Glu Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp
785 790 795 800

Gly Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile
805 810 815

Met Asp Arg Pro Pro Arg Ser Pro Lys Glu Pro Leu Ile Ser Gly Trp
820 825 830

Leu Phe Phe Arg Tyr Met Ala Ile Gly Gly Tyr Val Gly Ala Ala Thr
835 840 845

Val Gly Ala Ala Ala Trp Trp Phe Leu Tyr Ala Glu Asp Gly Pro His

850 855 860
Val Ser Tyr His Gln Leu Thr His Phe Met Gln Cys Thr Glu His Asn
865 870 875 880
Pro Glu Phe Asp Gly Leu Asp Cys Glu Val Phe Glu Ala Pro Glu Pro
885 890 895
Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala
900 905 910
Leu Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp
915 920 925
Val Asn Ile Trp Leu Leu Gly Ser Ile Cys Leu Ser Met Ser Leu His
930 935 940
Phe Leu Ile Leu Tyr Val Asp Pro Leu Pro Met Ile Phe Lys Leu Arg
945 950 955 960
Ala Leu Asp Phe Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro
965 970 975
Val Ile Gly Leu Asp Glu Leu Leu Lys Phe Ile Ala Arg Asn Tyr Leu
980 985 990
Glu Gly

<210> 15
<211> 998
<212> PRT
<213> Mus musculus

<400> 15
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Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu
20 25 30
Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr
35 40 45
Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
50 55 60
Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65 70 75 80
Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
85 90 95
Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
145 150 155 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
210 215 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val
225 230 235 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
245 250 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
260 265 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
275 280 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
290 295 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305 310 315 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
325 330 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
340 345 350

Thr Gly Thr Leu Thr Thr

SEQUENCE LISTING

<110> CHRISTENSEN, GEIR
ANDERSSON, KRISTIN BREVIK

<120> NON-HUMAN MAMMAL COMPRISING A MODIFIED SERCA2 GENE AND
METHODS, CELLS, GENES, AND VECTORS THEREOF

<130> 3657-1037

<140> 10585077
<141> 2008-10-07

<150> PCT/NO04/000397

<151> 2004-12-22

<150> 60/533,740

<151> 2003-12-30

<160> 32

<170> PatentIn Ver. 3.3

<210> 1
<211> 801
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 1

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acccggctcc acctctgtggg gcttggctcg ggcgc当地 cgc当地 gagaggccgg 180
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<210> 2
<211> 803
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

nucleotide construct

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gtttaagtct gaccagggg gatccggAAC ccttaatata acttcgtata atgtatgcta 180
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ggaagcggca gcccattcgc cgccaaGCTCA tttcagcaat atcacgggta gccaacgcta 660
tgtctgataa gcggtccgccc cacacccaaac cggccacaag tcatgaaatc caaaaaagcg 720
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<210> 3

<211> 860

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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cgtagacgat atcgtcgcgc gaacccaggg ccaccagcaa gttgcgttgt ggtgggtttc 180
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caggcctggg tggagaggct ttttgcctcc tcttgcaaaa ccacactgct cgacattggg 660
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tgaaaacatt agcttagagg 860

<210> 4

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 4

ataacttcgt ataatgtatg ctatacgaag ttat

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 5
ccaaggaaga tggctgacc 19

<210> 6
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<223> Description of Artificial Sequence: Synthetic primer

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catcgacgcc tcataaatcc 20

<210> 7
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<210> 9
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<213> Artificial Sequence
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<400> 9
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<210> 10
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic primer

<400> 10
aagttgaata accggaaatg gttt

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<210> 11
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<223> Description of Artificial Sequence: Synthetic primer

<400> 11
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<210> 12
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<400> 12
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<210> 13
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<223> Description of Artificial Sequence: Synthetic primer

<400> 13

gtaagagagc ttcccttcctc ctt

23

<210> 14

<211> 994

<212> PRT

<213> Mus musculus

<400> 14

Met Glu Ala Ala His Ser Lys Ser Thr Glu Glu Cys Leu Ser Tyr Phe
1 5 10 15

Gly Val Ser Glu Thr Thr Gly Leu Thr Pro Asp Gln Val Lys Arg His
20 25 30

Leu Glu Lys Tyr Gly Pro Asn Glu Leu Pro Ala Glu Glu Gly Lys Ser
35 40 45

Leu Trp Glu Leu Val Val Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
50 55 60

Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65 70 75 80

Gly Glu Glu Thr Val Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
85 90 95

Ile Leu Ile Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125

Val Tyr Arg Ala Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Arg Asp
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Val Ala Val Gly Asp Lys Val Pro
145 150 155 160

Ala Asp Ile Arg Ile Leu Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Val Gly Ile Val Ala
210 215 220

Thr Thr Gly Val Ser Thr Glu Ile Gly Lys Ile Arg Asp Gln Met Ala
225 230 235 240

Ala Thr Glu Gln Asp Lys Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe

	245	250	255
Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Val Ala Val Trp			
260	265	270	
Leu Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp			
275	280	285	
Phe Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val			
290	295	300	
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala			
305	310	315	320
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu			
325	330	335	
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys			
340	345	350	
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Lys Met Phe Ile			
355	360	365	
Ile Asp Lys Val Asp Gly Asp Val Cys Ser Leu Asn Glu Phe Ser Ile			
370	375	380	
Thr Gly Ser Thr Tyr Ala Pro Glu Gly Glu Val Leu Lys Asn Asp Lys			
385	390	395	400
Pro Val Arg Ala Gly Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile			
405	410	415	
Cys Ala Leu Cys Asn Asp Ser Ser Leu Asp Phe Asn Glu Thr Lys Gly			
420	425	430	
Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Thr Leu			
435	440	445	
Val Glu Lys Met Asn Val Phe Asn Thr Glu Val Arg Ser Leu Ser Lys			
450	455	460	
Val Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Arg Gln Leu Met Lys			
465	470	475	480
Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val			
485	490	495	
Tyr Cys Ser Pro Ala Lys Ser Ser Arg Ala Ala Val Gly Asn Lys Met			
500	505	510	
Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Asn Tyr Val			
515	520	525	
Arg Val Gly Thr Thr Arg Val Pro Leu Thr Gly Pro Val Lys Glu Lys			
530	535	540	
Ile Met Ser Val Ile Lys Glu Trp Gly Thr Gly Arg Asp Thr Leu Arg			

545 550 555 560
Cys Leu Ala Leu Ala Thr Arg Asp Thr Pro Pro Lys Arg Glu Glu Met
565 570 575

Val Leu Asp Asp Ser Ala Lys Phe Met Glu Tyr Glu Met Asp Leu Thr
580 585 590

Phe Val Gly Val Val Gly Met Leu Asp Pro Pro Arg Lys Glu Val Thr
595 600 605

Gly Ser Ile Gln Leu Cys Arg Asp Ala Gly Ile Arg Val Ile Met Ile
610 615 620

Thr Gly Asp Asn Lys Gly Thr Ala Ile Ala Ile Cys Arg Arg Ile Gly
625 630 635 640

Ile Phe Ser Glu Asn Glu Glu Val Thr Asp Arg Ala Tyr Thr Gly Arg
645 650 655

Glu Phe Asp Asp Leu Pro Leu Ala Glu Gln Arg Glu Ala Cys Arg Arg
660 665 670

Ala Cys Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val
675 680 685

Glu Tyr Leu Gln Ser Tyr Asp Glu Ile Thr Ala Met Thr Gly Asp Gly
690 695 700

Val Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met
705 710 715 720

Gly Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala
725 730 735

Asp Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala
740 745 750

Ile Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn
755 760 765

Val Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Leu Pro
770 775 780

Glu Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp
785 790 795 800

Gly Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile
805 810 815

Met Asp Arg Pro Pro Arg Ser Pro Lys Glu Pro Leu Ile Ser Gly Trp
820 825 830

Leu Phe Phe Arg Tyr Met Ala Ile Gly Gly Tyr Val Gly Ala Ala Thr
835 840 845

Val Gly Ala Ala Ala Trp Trp Phe Leu Tyr Ala Glu Asp Gly Pro His

850 855 860
Val Ser Tyr His Gln Leu Thr His Phe Met Gln Cys Thr Glu His Asn
865 870 875 880
Pro Glu Phe Asp Gly Leu Asp Cys Glu Val Phe Glu Ala Pro Glu Pro
885 890 895
Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala
900 905 910
Leu Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp
915 920 925
Val Asn Ile Trp Leu Leu Gly Ser Ile Cys Leu Ser Met Ser Leu His
930 935 940
Phe Leu Ile Leu Tyr Val Asp Pro Leu Pro Met Ile Phe Lys Leu Arg
945 950 955 960
Ala Leu Asp Phe Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro
965 970 975
Val Ile Gly Leu Asp Glu Leu Leu Lys Phe Ile Ala Arg Asn Tyr Leu
980 985 990
Glu Gly

<210> 15
<211> 998
<212> PRT
<213> Mus musculus

<400> 15
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1 5 10 15
Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu
20 25 30
Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr
35 40 45
Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
50 55 60
Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65 70 75 80
Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
85 90 95
Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
145 150 155 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
165 170 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
180 185 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
210 215 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val
225 230 235 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
245 250 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
260 265 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
275 280 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
290 295 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305 310 315 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
325 330 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
340 345 350

Thr Gly Thr Leu Thr Thr